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 NEWS  5  AUG 13   Field Availability (/FA) field enhanced in BEILSTEIN
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 NEWS  7  AUG 18   Simultaneous left and right truncation added to PASCAL
 NEWS  8  AUG 18   FROSTI and KOSMET enhanced with Simultaneous Left and Righ
                   Truncation
 NEWS  9  AUG 18   Simultaneous left and right truncation added to ANABSTR
 NEWS 10  SEP 22   DIPPR file reloaded
 NEWS 11  SEP 25   INPADOC: Legal Status data to be reloaded
 NEWS 12  SEP 29   DISSABS now available on STN
 NEWS 13  OCT 10   PCTFULL: Two new display fields added
 NEWS 14  OCT 21   BIOSIS file reloaded and enhanced
 NEWS 15  OCT 28   BIOSIS file segment of TOXCENTER reloaded and enhanced

 NEWS EXPRESS  NOVEMBER 14 CURRENT WINDOWS VERSION IS V6.01c, CURRENT
               MACINTOSH VERSION IS V6.0b(ENG) AND V6.0Jb(JP),
               AND CURRENT DISCOVER FILE IS DATED 23 SEPTEMBER 2003
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=> file biosis, wpids, fsta, medline,
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                                                       ENTRY    SESSION
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FILE 'MEDLINE' ENTERED AT 16:18:40 ON 18 NOV 2003

=> s prokaryotic elongation factor p or efp
L1          358 PROKARYOTIC ELONGATION FACTOR P OR EFP

=> s oxazolidinone compound
L2          121 OXAZOLIDINONE COMPOUND

=> s l1 and l2
L3            1 L1 AND L2

=> d l3 ti abs ibib tot

L3   ANSWER 1 OF 1  WPIDS  COPYRIGHT 2003 THOMSON DERWENT on STN
TI   Identifying a compound which modulates the activity of prokaryotic
     elongation factor p (efp) for
     screening for compounds which can be used as antibiotics comprises
     contacting efp with a compound and determining if efp
     activity is modified.
AN   2000-524303 [47]   WPIDS
AB   WO 200045177 A UPAB: 20000925
     NOVELTY - A method (M1) for identifying a compound which modulates the
     activity of efp comprises contacting efp with a
     compound and determining whether the compound modifies activity of
     efp.
          DETAILED DESCRIPTION - INDEPENDENT CLAIMS are also included for the
     following:
          (1) a method (M2) for identifying a compound which modulates
      fp activity comprising:
          (a) contacting a cell containing efp with a compound
     identified by M1; and
          (b) determining whether the compound inhibits cell growth;
          (2) a method (M3) for identifying a compound which modulates
     efp activity comprising:
          (a) contacting a composition comprising efp,
     N-formylmethionyl-tRNA (fMet-tRNA), 30S subunit, 50S, an mRNA containing
     an AUG sequence and initiation factors 1,2 and 3 with a compound; and
          (b) determining whether the compound allows fMet-tRNA to bind to a
     complex formed through the interaction of efp, 30S subunit, 50S,
     an mRNA containing an AUG sequence and initiation factors 1,2 and 3;
          (3) a method (M4) for identifying a compound which modulates
     efp activity comprising:
          (a) contacting efp with prokaryotic 30S subunit or 70S
     ribosome to form a composition;
          (b) contacting the composition with a compound; and
          (c) determining whether the compound binds to efp in
     association with the 30S  subunit or 70S ribosome or interferes with the
     binding of efp and the 30S  subunit or 70S ribosome;
          (4) a method (M5) for identifying a compound which modulates
     efp activity comprising:
          (a) contacting efp with a composition comprising either 50S
     subunit or 70S ribosome, a tRNA fragment comprising CACCA-radiolabeled
     amino acid and a peptide bond donor to form a second composition;
          (b) contacting the second composition with the compound; and
          (c) determining whether the compound inhibits the first peptide bond
     reaction;
          (5) a method (M6) for identifying a compound which modulates
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efp activity comprising:

(a) contacting a cell or composition containing **efp** with a detectably labelled **oxazolidinone compound** known to bind **efp**;

(b) contacting the composition or cell with an unlabelled compound; and

(c) determining whether the unlabelled compound displaces the labelled **oxazolidinone compound** from the complex;

(6) a method (M7) for identifying a compound which modulates **efp** but not eukaryotic eIF5A activity comprising:

(a) determining whether the compound modulates the activity of prokaryotic **efp** by M1 - M7;

(b) contacting eIF5A with a composition comprising methionyl-tRNA (Met-tRNA), 80S ribosome, an mRNA containing an AUG sequence, initiation factors eIF-2, eIF-3, eIF-5, eIF-4C, eIF-4D and a peptide bond donor to form a second composition;

(c) contacting the second composition with a compound; and

(d) determining whether the compound inhibits the first peptide bond reaction of a complex formed through the interaction of eIF5A, Met-tRNA, 80S ribosome, an mRNA containing an AUG sequence, initiation factors eIF-2, eIF-3, eIF-5, eIF-4C and eIF-4D; and

(7) modulating the activity of prokaryotic **efp**, the 30S subunit, 50S subunit, 70S ribosome or L16 protein comprising contacting the **efp** or cell or cell preparation containing the **efp** , the 30S subunit, 50S subunit, 70S ribosome or L16 protein with an **oxazolidinone compound**.

USE - To screen for compounds which modulate ribosome mediated peptide bond formation. These screening assays can be used to discover new and useful antibiotics.

ADVANTAGE - This screening method is more rapid and direct than currently available methods.

Dwg.0/0

ACCESSION NUMBER: 2000-524303 [47] WPIDS
DOC. NO. NON-CPI: N2000-387540
DOC. NO. CPI: C2000-155724
TITLE: Identifying a compound which modulates the activity of **prokaryotic elongation factor p** (**efp**) for screening for compounds which can be used as antibiotics comprises contacting **efp** with a compound and determining if **efp** activity is modified.
DERWENT CLASS: B04 D16 S03
INVENTOR(S): MAROTTI, K R; POORMAN, R A; SHINABARGER, D L; WELLS, P A
PATENT ASSIGNEE(S): (PHAA) PHARMACIA & UPJOHN; (PHAA) PHARMACIA & UPJOHN CO
COUNTRY COUNT: 87
PATENT INFORMATION:

PATENT NO	KIND	DATE	WEEK	LA	PG
WO 2000045177	A1	20000803	(200047)*	EN	52
RW: AT BE CH CY DE DK EA ES FI FR GB GH GM GR IE IT KE LS LU MC MW NL OA PT SD SE SL SZ UG ZW					
W: AE AL AM AT AU AZ BA BB BG BR BY CA CH CN CU CZ DE DK EE ES FI GB GD GE GH GM HR HU ID IL IN IS JP KE KG KP KR KZ LC LK LR LS LT LU LV MD MG MK MN MW MX NO NZ PL PT RO RU SD SE SG SI SK SL TJ TM TR TT UA UG US UZ VN YU ZA ZW					
AU 9942246	A	20000818	(200057)		
EP 1147422	A1	20011024	(200171)	EN	
R: AL AT BE CH CY DE DK ES FI FR GB GR IE IT LI LT LU LV MC MK NL PT RO SE SI					
JP 2002535680	W	20021022	(200301)		63
US 6511813	B1	20030128	(200311)		

APPLICATION DETAILS:

PATENT NO	KIND		APPLICATION	DATE
WO 2000045177	A1		WO 1999-US12073	19990528
AU 9942246	A		AU 1999-42246	19990528
EP 1147422	A1		EP 1999-926086	19990528
			WO 1999-US12073	19990528
JP 2002535680	W		WO 1999-US12073	19990528
			JP 2000-596378	19990528
US 6511813	B1	Provisional	US 1999-117473P	19990127
		Div ex	US 1999-322732	19990528
			US 2000-704321	20001102

FILING DETAILS:

PATENT NO	KIND		PATENT NO
AU 9942246	A	Based on	WO 2000045177
EP 1147422	A1	Based on	WO 2000045177
JP 2002535680	W	Based on	WO 2000045177

PRIORITY APPLN. INFO: US 1999-117473P 19990127; US 1999-322732 19990528; US 2000-704321 20001102

=> s efp and protein
L4 81 EFP AND PROTEIN

=> s l4 and activity
L5 23 L4 AND ACTIVITY

=> d l5 ti abs ibib tot

L5 ANSWER 1 OF 23 BIOSIS COPYRIGHT 2003 BIOLOGICAL ABSTRACTS INC. on STN
TI The chvH locus of Agrobacterium encodes a homologue of an elongation factor involved in **protein** synthesis.
AB The virulence of Agrobacterium tumefaciens depends on both chromosome- and Ti plasmid-encoded gene products. In this study, we characterize a chromosomal locus, chvH, previously identified by TnphoA mutagenesis and shown to be required for tumor formation. Through DNA sequencing and comparison of the sequence with identified sequences in the database, we show that this locus encodes a **protein** similar in sequence to elongation factor P, a **protein** thought to be involved in peptide bond synthesis in Escherichia coli. The analysis of vir-lacZ and vir-phoA translational fusions as well as Western immunoblotting revealed that the expression of Vir proteins such as VirE2 was significantly reduced in the chvH mutant compared with the wild-type strain. The E. coli **efp** gene complemented detergent sensitivity, virulence, and expression of VirE2 in the chvH mutant, suggesting that chvH and **efp** are functionally homologous. As expected, ChvH exerts its **activity** at the posttranscriptional level. Southern analysis suggests that the gene encoding this elongation factor is present as a single copy in A. tumefaciens. We constructed a chvH deletion mutant in which a 445-bp fragment within its coding sequence was deleted and replaced with an omega fragment. On complex medium, this mutant grew more slowly than the wild-type strain, indicating that elongation factor P is important but not essential for the growth of Agrobacterium.
ACCESSION NUMBER: 2001:61207 BIOSIS
DOCUMENT NUMBER: PREV200100061207
TITLE: The chvH locus of Agrobacterium encodes a homologue of an elongation factor involved in **protein** synthesis.
AUTHOR(S): Peng, Wen-Tao; Banta, Lois M.; Charles, Trevor C.; Nester, Eugene W. [Reprint author]
CORPORATE SOURCE: Department of Microbiology, University of Washington,

Seattle, WA, 98195-7242, USA
gnester@u.washington.edu
SOURCE: Journal of Bacteriology, (January, 2001) Vol. 183, No. 1, pp. 36-45. print.
CODEN: JOBAAY. ISSN: 0021-9193.
DOCUMENT TYPE: Article
LANGUAGE: English
ENTRY DATE: Entered STN: 31 Jan 2001
Last Updated on STN: 12 Feb 2002

L5 ANSWER 2 OF 23 BIOSIS COPYRIGHT 2003 BIOLOGICAL ABSTRACTS INC. on STN
TI A novel baculovirus envelope fusion **protein** with a proprotein convertase cleavage site.
AB The entry mechanism of Spodoptera exigua multicapsid nucleopolyhedrovirus (SeMNPV), a group II NPV, in cultured cells was examined. SeMNPV budded virus (BV) enters by endocytosis as do the BVs of the group I NPVs, Autographa californica (Ac) MNPV and Orgyia pseudotsugata (Op) MNPV. In group I NPVs, upon infection acidification of the endosome triggers fusion of the viral and endosomal membrane, which is mediated by the BV envelope glycoprotein GP64. However, the SeMNPV genome lacks a homolog of GP64 envelope fusion **protein** (**EFP**). A functional homolog of the OpMNPV GP64 **EFP** was identified in SeMNPV ORF8 (Se8; 76 kDa) and appeared to be the major BV envelope **protein**. Surprisingly, a 60-kDa cleavage product of this **protein** is present in the BV envelope. A furin-like proprotein convertase cleavage site (R-X-K/R-R) was identified immediately upstream of the N-terminus of the mature Se8 **protein** and this site was also conserved in the Lymantria dispar (Ld) MNPV homolog (Ld130) of Se8. Syncytium formation assays showed that Se8 and Ld130 alone were sufficient to mediate membrane fusion upon acidification of the medium. Furthermore, C-terminal GFP-fusion proteins of Se8 and Ld130 were primarily localized in the plasma membrane of insect cells. This is consistent with their fusogenic **activity** and supports the conclusion that the Se8 gene product is a functional homolog of the GP64 **EFP**.
ACCESSION NUMBER: 2000:469691 BIOSIS
DOCUMENT NUMBER: PREV200000469691
TITLE: A novel baculovirus envelope fusion **protein** with a proprotein convertase cleavage site.
AUTHOR(S): IJkel, Wilfred F. J.; Westenberg, Marcel; Goldbach, Rob W.; Blissard, Gary W.; Vlak, Just M. [Reprint author]; Zuidema, Douwe
CORPORATE SOURCE: Laboratory of Virology, Wageningen University and Research Center, Binnenhaven 11, 6709 PD, Wageningen, Netherlands
SOURCE: Virology, (September 15, 2000) Vol. 275, No. 1, pp. 30-41. print.
CODEN: VIRLAX. ISSN: 0042-6822.
DOCUMENT TYPE: Article
LANGUAGE: English
ENTRY DATE: Entered STN: 1 Nov 2000
Last Updated on STN: 10 Jan 2002

L5 ANSWER 3 OF 23 BIOSIS COPYRIGHT 2003 BIOLOGICAL ABSTRACTS INC. on STN
TI Interferon stimulating **protein** and uses thereof.
AB This invention relates to the use of the baculovirus glycoprotein, Interferon Stimulating **Protein** (ISP) (also known as gp67, gp64 **EFP**, or gp64), or the gene sequence encoding ISP, to stimulate production of interferon, such as for immunotherapy, anti-viral, anti-cancer, anti-bacterial, or anti-parasitic therapy. This invention also relates to novel mutant forms of ISP that show enhanced biological (i.e., anti-viral) **activity**, increased stability, higher yield or better solubility.
ACCESSION NUMBER: 2000:290863 BIOSIS
DOCUMENT NUMBER: PREV200000290863
TITLE: Interferon stimulating **protein** and uses thereof.

AUTHOR(S): Hilbert, David M. [Inventor]; Bednarik, Daniel P. [Inventor, Reprint author]; Nardelli, Bernadett [Inventor]; Murphy, Marianne [Inventor]; Parmelee, David [Inventor]; Gronowski, Ann [Inventor]; Schreiber, Robert [Inventor]
CORPORATE SOURCE: Columbia, MD, USA
ASSIGNEE: Humn Genome Sciences, Inc., Rockville, MD, USA; Washington University
PATENT INFORMATION: US 6001806 December 14, 1999
SOURCE: Official Gazette of the United States Patent and Trademark Office Patents, (Dec. 14, 1999) Vol. 1229, No. 2. e-file.
CODEN: OGUPE7. ISSN: 0098-1133.
DOCUMENT TYPE: Patent
LANGUAGE: English
ENTRY DATE: Entered STN: 6 Jul 2000
Last Updated on STN: 7 Jan 2002

L5 ANSWER 4 OF 23 BIOSIS COPYRIGHT 2003 BIOLOGICAL ABSTRACTS INC. on STN
TI **Efp** as a primary estrogen-responsive gene in human breast cancer.
AB We have previously isolated the **efp** (estrogen-responsive finger **protein**) that is required for the normal estrogen-induced cell proliferation. Here, we show the genomic organization of the human **efp** gene which consists of nine exons. The **efp** mRNA was expressed in human breast tumors and the estrogen-induced expression of the **efp** was found in MCF-7 human breast cancer cells. Moreover, **efp** promoter **activity** was enhanced through the estrogen-responsive element dependent on estrogen and estrogen receptor. These results suggest that the **efp** can mediate estrogen actions such as cell growth in human breast cancer as a primary responsive gene.
ACCESSION NUMBER: 2000:252423 BIOSIS
DOCUMENT NUMBER: PREV200000252423
TITLE: **Efp** as a primary estrogen-responsive gene in human breast cancer.
AUTHOR(S): Ikeda, Kazuhiro; Orimo, Akira; Higashi, Yasuhiro; Muramatsu, Masami; Inoue, Satoshi [Reprint author]
CORPORATE SOURCE: Department of Biochemistry, Saitama Medical School, 38 Morohongo, Moroyama, Iruma-gun, Saitama, 350-0495, Japan
SOURCE: FEBS Letters, (April 21, 2000) Vol. 472, No. 1, pp. 9-13. print.
CODEN: FEBLAL. ISSN: 0014-5793.
DOCUMENT TYPE: Article
LANGUAGE: English
ENTRY DATE: Entered STN: 14 Jun 2000
Last Updated on STN: 5 Jan 2002

L5 ANSWER 5 OF 23 BIOSIS COPYRIGHT 2003 BIOLOGICAL ABSTRACTS INC. on STN
TI Estrogen-responsive RING finger mRNA induction in gastrointestinal carcinoma cells following bile acid treatment.
AB The underlying molecular mechanisms of the tumor-promoting **activity** of bile acids such as chenodeoxycholic acid (CDCA) and deoxycholic acid (DCA) and the protective effect of ursodeoxycholic acid (UDCA) remain largely unclear. Using RNA arbitrarily primed PCR (RAP-PCR) for differential display, we identified, cloned and sequenced differentially expressed transcripts after treating gastric carcinoma cells (St 23132) with the bile acids CDCA, DCA and UDCA. One of these transcripts was identified to be an estrogen-responsive RING finger **protein** (**efp**) mRNA. The differential expression of **efp** in gastric cancer cells was confirmed by low stringency RT-PCR. **efp** mRNA levels were induced 3-fold in gastric carcinoma cells after CDCA and DCA treatment, whereas no change in expression was detected after UDCA treatment. Finally, treatment of the colon carcinoma cell line HT 29 with DCA resulted in a 2- to 5-fold induction of **efp** mRNA levels whereas UDCA did not induce **efp**. As expected, **efp** expression was also increased after 24 h of

estrogen treatment. In summary, a synergy or a common pathway of tumor enhancement of bile acids and estrogen via **efp** in gastrointestinal carcinogenesis can be envisioned.

ACCESSION NUMBER: 1999:41887 BIOSIS
DOCUMENT NUMBER: PREV199900041887
TITLE: Estrogen-responsive RING finger mRNA induction in gastrointestinal carcinoma cells following bile acid treatment.
AUTHOR(S): Jung, Barbara; Vogt, Thomas; Mathieu-Daude, Francoise; Welsh, John; McClelland, Michael; Trenkle, Thomas; Weitzel, Christoph; Kullmann, Frank [Reprint author]
CORPORATE SOURCE: Dep. Internal Med. I, Univ. Regensburg, 93042 Regensburg, Germany
SOURCE: Carcinogenesis (Oxford), (Nov., 1998) Vol. 19, No. 11, pp. 1901-1906. print.
CODEN: CRNGDP. ISSN: 0143-3334.
DOCUMENT TYPE: Article
LANGUAGE: English
ENTRY DATE: Entered STN: 3 Feb 1999
Last Updated on STN: 3 Feb 1999

L5 ANSWER 6 OF 23 BIOSIS COPYRIGHT 2003 BIOLOGICAL ABSTRACTS INC. on STN
TI Promoter analysis of mouse estrogen-responsive finger **protein** (**efp**) gene: Mouse **efp** promoter contains an E-box that is also conserved in human.
AB The estrogen-responsive finger **protein** (**efp**) containing a RING finger motif has been identified as an estrogen-responsive gene in human and mouse. Here, we have characterized the basal promoter region of the mouse **efp** gene. The promoter lacks the TATA motif, and transcription initiation sites are found at positions - 38T, - 64A and - 73C from the translation initiation site. Deletion analysis of the 5'-flanking region using Jyg-Mc(B) mouse breast cancer cells indicates that the sequence encompassing from - 139 to - 1 has a basal transcription **activity**. This region is GC-rich in both mouse and human promoters, and the E-box is precisely matched on the sequence alignment. A mutation experiment with E-box shows that the E-box is functionally active. An electrophoretic mobility shift assay using Jyg-Mc(B) nuclear extracts shows that a transcription factor, USF-1 binds to the E-box in the mouse **efp** promoter. It has been shown that the E-box in the human **efp** promoter is indispensable for basal transcriptional **activity** and binds USF-1. These findings suggest that the mouse **efp** promoter is regulated by a similar mechanism to that of the human. In mouse, however, we have not found a negative regulatory region that is present in human promoter.

ACCESSION NUMBER: 1998:433130 BIOSIS
DOCUMENT NUMBER: PREV199800433130
TITLE: Promoter analysis of mouse estrogen-responsive finger **protein** (**efp**) gene: Mouse **efp** promoter contains an E-box that is also conserved in human.
AUTHOR(S): Ikeda, Kazuhiro; Inoue, Satoshi; Orimo, Akira; Tsutsumi, Ken-Ichi; Muramatsu, Masami [Reprint author]
CORPORATE SOURCE: Dep. Biochem., Saitama Med. Sch., Moroyama, Saitama 350-04, Japan
SOURCE: Gene (Amsterdam), (Aug. 17, 1998) Vol. 216, No. 1, pp. 155-162. print.
CODEN: GENED6. ISSN: 0378-1119.
DOCUMENT TYPE: Article
LANGUAGE: English
ENTRY DATE: Entered STN: 7 Oct 1998
Last Updated on STN: 7 Oct 1998

L5 ANSWER 7 OF 23 BIOSIS COPYRIGHT 2003 BIOLOGICAL ABSTRACTS INC. on STN
TI The gene encoding the elongation factor P **prot in** is essential for viability and is required for **protein** synthesis.

AB Elongation factor P (**EFP**) is a **protein** that stimulates the peptidyltransferase **activity** of fully assembled 70 S prokaryotic ribosomes and enhances the synthesis of certain dipeptides initiated by N-formylmethionine. This reaction appears conserved throughout species and is promoted in eukaryotic cells by a homologous **protein**, eIF5A. Here we ask whether the Escherichia coli gene encoding **EFP** is essential for cell viability. A kanamycin resistance (KanR) gene was inserted near the N-terminal end of the **efp** gene and was cloned into a plasmid, pMAK705, that has a temperature-sensitive origin of replication. After transformation into a recA+ E. coli strain, temperature-sensitive mutants were isolated, and their chromosomal DNA was sequenced. Mutants containing the **efp** -KanR gene in the chromosome grew at 33degree C only in the presence of the wild-type copy of the **efp** gene in the pMAK705 plasmid and were unable to grow at 44degree C. Incorporation of various isotopes in vivo suggests that translation is impaired in the **efp** mutant at 44degree C. At 44degree C, mutant cells are severely defective in peptide-bond formation. We conclude that the **efp** gene is essential for cell viability and is required for **protein** synthesis.

ACCESSION NUMBER: 1998:83503 BIOSIS
DOCUMENT NUMBER: PREV199800083503
TITLE: The gene encoding the elongation factor P **protein** is essential for viability and is required for **protein** synthesis.
AUTHOR(S): Aoki, Hiroyuki; Dekany, Katalin; Adams, Sally-Lin; Ganoza, M. Clelia [Reprint author]
CORPORATE SOURCE: C.H. Best Inst., Univ. Toronto, Toronto, ON M5G 1L6, Canada
SOURCE: Journal of Biological Chemistry, (Dec. 19, 1997) Vol. 272, No. 51, pp. 32254-32259. print.
CODEN: JBCHA3. ISSN: 0021-9258.
DOCUMENT TYPE: Article
LANGUAGE: English
ENTRY DATE: Entered STN: 24 Feb 1998
Last Updated on STN: 24 Feb 1998

L5 ANSWER 8 OF 23 BIOSIS COPYRIGHT 2003 BIOLOGICAL ABSTRACTS INC. on STN
TI Multiple regulatory elements and binding proteins of the 5'-flanking region of the human estrogen-responsive finger **protein** (**efp**) gene.
AB The **efp**, a member of the RING finger family, was previously identified as an estrogen responsive gene. Here, we characterized basal promoter of the human **efp** gene. Transcription initiation site was found at position -60 G relative to the site for translation initiation, and TATA motif was absent. Deletion and mutation analyses of the 5'-flanking region using MCF-7 breast cancer cells indicated that the sequences located at -137 to -72 had the promoter **activity** for which an E-box (CACGTG) element at -110 to -105 was essential. EMSA showed that USF-1 bound to the E-box and that a **protein**-DNA complex was formed at the positive regulatory region (-137 to -110). Moreover, a strong negative regulatory region was present in -235 to -174. These findings suggest that the human **efp** promoter is regulated by multiple elements and their interacting factors, and the E-box near the transcription initiation site is essential for the basal promoter **activity**.

ACCESSION NUMBER: 1997:438717 BIOSIS
DOCUMENT NUMBER: PREV199799737920
TITLE: Multiple regulatory elements and binding proteins of the 5'-flanking region of the human estrogen-responsive finger **protein** (**efp**) gene.
AUTHOR(S): Ikeda, Kazuhiro; Inoue, Satoshi; Orimo, Akira; Sano, Michio; Watanabe, Toru; Tsutsumi, Kenichi; Muramatsu, Masami [Reprint author]
CORPORATE SOURCE: Dep. Biochemistry, Saitama Med. Sch., Moroyama, Saitama

350-04, Japan
SOURCE: Biochemical and Biophysical Research Communications, (1997) Vol. 236, No. 3, pp. 765-771.
CODEN: BBRCA9. ISSN: 0006-291X.
DOCUMENT TYPE: Article
LANGUAGE: English
ENTRY DATE: Entered STN: 8 Oct 1997
Last Updated on STN: 8 Oct 1997

L5 ANSWER 9 OF 23 BIOSIS COPYRIGHT 2003 BIOLOGICAL ABSTRACTS INC. on STN
TI Identification of a membrane fusion domain and an oligomerization domain in the baculovirus GP64 envelope fusion **protein**.
AB The baculovirus GP64 envelope fusion **protein** (GP64 **EFP**) is the major envelope glycoprotein of the budded virion and has been shown to mediate acid-triggered membrane fusion both in virions and when expressed alone in transfected cells. Using site-directed mutagenesis and functional assays for oligomerization, transport, and membrane fusion, we localized two functional domains of GP64 **EFP**. To identify a fusion domain in the GP64 **EFP** of the Orgyia pseudotsugata multiple nuclear polyhedrosis virus (OpMNPV), we examined two hydrophobic regions in the GP64 **EFP** ectodomain. Hydrophobic region I (amino acids 223 to 228) is a cluster of 6 hydrophobic amino acids exhibiting the highest local hydrophobicity in the ectodomain. Hydrophobic region II (amino acids 330 to 338) lies within a conserved region of GP64 **EFP** that contains a heptad repeat of leucine residues and is predicted to form an amphipathic alpha-helix. In region I, nonconservative amino acid substitutions at Leu-226 and Leu-227 (at the center of the hydrophobic cluster) completely abolished fusion **activity** but did not prevent GP64 **EFP** oligomerization or surface localization. To confirm the role of region I in membrane fusion **activity**, we used a synthetic 21-amino-acid peptide to generate polyclonal antibodies against region I and demonstrated that antipeptide antibodies were capable of both neutralizing membrane fusion **activity** and reducing infectivity of the virus. In hydrophobic region II, mutations were designed to disrupt several structural characteristics: a heptad repeat of leucine, a predicted alpha-helix, or the local hydrophobicity along one face of the helix. Single alanine substitutions for heptad leucines did not prevent oligomerization, transport, or fusion **activity**. However, multiple alanine substitutions or proline (helix-destabilizing) substitutions disrupted both oligomerization and transport of GP64 **EFP**. In addition, a deletion that removed region II and the predicted alpha-helix was defective for oligomerization, whereas a larger deletion that retained region II and the predicted helix was oligomerized. These results indicate that region II is required for oligomerization and transport and suggest that the predicted helical structure of this region may be important for this function. Thus, by using mutagenesis, functional assays, and antibody inhibition, two functional domains were localized within the baculovirus GP64 **EFP**: a fusion domain located at amino acids 223 to 228 and an oligomerization domain located at amino acids 327 to 335 within a predicted amphipathic alpha-helix.
ACCESSION NUMBER: 1995:182951 BIOSIS
DOCUMENT NUMBER: PREV199598197251
TITLE: Identification of a membrane fusion domain and an oligomerization domain in the baculovirus GP64 envelope fusion **protein**.
AUTHOR(S): Monsma, Scott A.; Blissard, Gary W. [Reprint author]
CORPORATE SOURCE: Boyce Thompson Inst., Cornell Univ., Tower Road, Ithaca, NY 14853-1801, USA
SOURCE: Journal of Virology, (1995) Vol. 69, No. 4, pp. 2583-2595.
CODEN: JOVIAM. ISSN: 0022-538X.
DOCUMENT TYPE: Article
LANGUAGE: English
ENTRY DATE: Entered STN: 26 Apr 1995

Last Updated on STN: 26 Apr 1995

L5 ANSWER 10 OF 23 BIOSIS COPYRIGHT 2003 BIOLOGICAL ABSTRACTS INC. on STN
TI Overlapping TATA-dependent and TATA-independent early promoter activities in the baculovirus gp64 envelope fusion **protein** gene.
AB In previous studies to characterize basal and activated transcription from the early promoter of the gp64 envelope fusion **protein** (**efp**) gene of the Orgyia pseudotsugata multicapsid nuclear polyhedrosis virus. the TATA box was identified as a functional element, essential for basal transcription from a minimal promoter construct. In the current study, we used discrete deletions and multiple point mutations that removed the functional TATA box from larger promoter constructs of the gp64 **efp** gene to reveal an overlapping TATA-independent transcriptional **activity**. TATA-independent transcriptional **activity** was inhibited in vitro by alpha-amanitin but not by tagetitoxin, demonstrating that like the TATA-dependent **activity** the TATA-independent **activity** is mediated by RNA polymerase II. Using constructs in which the TATA box (TATATAA) was destroyed by substitution mutations, we identified four elements that are required for the TATA-independent **activity**. Two of the required elements, GATA (at -114) and CACGTG (at -104). were previously shown to specifically bind host transcription factors and activate transcription.from the TATA-dependent wild-type gp64 **efp** promoter. The role of the early start site consensus CAGT sequence in TATA-independent transcription was also examined. Single-nucleotide substitution mutations in the CAGT sequence indicated that certain nucleotides within the CAGT start site were essential. In addition to the start site sequence and two upstream elements, a fourth essential element was identified in the 5' untranslated leader region (5'UTR). While the 5'UTR was not necessary for TATA-dependent transcription, deletion of a 10-bp 5'UTR sequence resulted in the loss of TATA-independent transcriptional **activity**. Although necessary, neither the GATA, CACGTG, start site region, nor 5'UTR element was alone sufficient for accurately initiated TATA-independent transcription from the consensus CAGT start site. Thus, the gp64 **efp** early promoter contains overlapping TATA-dependent and TATA-independent transcriptional activities. A number of common sequence elements (GATA, CACGTG, and start site CAGT) are involved in both of these activities, while one element (in the 5'UTR) is required only in the TATA-independent context.
ACCESSION NUMBER: 1995:156675 BIOSIS
DOCUMENT NUMBER: PREV199598170975
TITLE: Overlapping TATA-dependent and TATA-independent early promoter activities in the baculovirus gp64 envelope fusion **protein** gene.
AUTHOR(S): Kogan, Philip H.; Chen, Xiaoying; Blissard, Gary W. [Reprint author]
CORPORATE SOURCE: Boyce Thompson Inst., Cornell, Tower Rd., Ithaca, NY 14853-1801, USA
SOURCE: Journal of Virology, (1995) Vol. 69, No. 3, pp. 1452-1461. CODEN: JOVIAM. ISSN: 0022-538X.
DOCUMENT TYPE: Article
LANGUAGE: English
ENTRY DATE: Entered STN: 11 Apr 1995
Last Updated on STN: 11 Apr 1995

L5 ANSWER 11 OF 23 WPIDS COPYRIGHT 2003 THOMSON DERWENT on STN
TI New crystallized recombinant polypeptides from Staphylococcus aureus, Streptococcus pneumoniae, Helicobacter pylori or Pseudomonas aeruginosa involved in general metabolism, useful as drug targets for pathogenic bacteria.
AN 2003-513596 [48] WPIDS
AB WO2003044185 A UPAB: 20030729
NOVELTY - A crystallized recombinant polypeptide (I) comprising the sequence of polypeptides from Staphylococcus aureus, Streptococcus

pneumoniae, Helicobacter pylori, Escherichia coli and Pseudomonas aeruginosa which are involved in general metabolism, or a sequence having at least 95% identity with the polypeptide sequence, where the polypeptide is in crystal form, is new.

DETAILED DESCRIPTION - A crystallized recombinant polypeptide (I) comprises the amino acid sequence (S) of polypeptides involved in general metabolism, which comprises:

(a) shikimate dehydrogenase (aroE) or **protein** chain elongation factor EF-Ts (tsf) from S. aureus;

(b) GroEL (mopA) from H. pylori;

(c) peptide deformylase (def), peptide chain release factor 1 (prfA), DnaK **protein** (heat shock **protein** (hsp) 70) (dnaK), or **protein** chain elongation factor EF-Tu (tufB) from P. aeruginosa;

(d) 3-phosphoshikimate 1-carboxyvinyltransferase (aroA), ribosome recycling factor (frr) or translation elongation factor P (**efp**) from S. pneumoniae; or

(e) DnaK **protein** (hsp 70) (dnaK) from E. coli, where the amino acid sequences are fully given in the specification.

(I) comprises an amino acid sequence having at least 95% identity with the amino acid sequence of the above polypeptide, or comprises an amino acid sequence encoded by a polynucleotide that hybridizes under stringent conditions to the complementary strand of a polynucleotide having a sequence encoding any of the above polypeptides. (I) is in a crystal form.

INDEPENDENT CLAIMS are also included for:

(1) a sample (II) comprising an isolated, recombinant polypeptide (P), comprising (S), an amino acid sequence having at least 95% identity with (S), or an amino acid sequence encoded by a polynucleotide that hybridizes under stringent conditions to the complementary strand of a polynucleotide having a sequence encoding (S), where (P) is labeled with a heavy atom, or is enriched in nuclear magnetic resonance (NMR) isotope;

(2) a crystallized complex comprising (I) and a co-factor or a small organic molecule, where the complex is in a crystal form;

(3) an isolated, recombinant polypeptide comprising an amino acid sequence having at least 90% identity with GroEL polypeptide from H. pylori, peptide deformylase from P. aeruginosa, 3-phosphoshikimate 1-carboxyvinyltransferase or ribosome recycling factor from S. pneumoniae, peptide chain release factor 1 from P. aeruginosa, or an amino acid sequence encoded by a polynucleotide that hybridizes under stringent conditions to the complementary strand of a polynucleotide encoding the above mentioned polypeptides, where the GroEL polypeptide comprises the amino acids residue K at position 58, T at position 307 and D at position 340, peptide deformylase comprises E at position 85, 3-phosphoshikimate 1-carboxyvinyltransferase comprises V at position 250 and C at position 307, ribosome recycling factor comprises L at position 88 and Q at position 142, and peptide chain release factor 1 comprises L at position 48, E at position 51 and V at position 304;

(4) a composition (III) comprising (P), where (P) is at least about 90% pure in a sample of (III);

(5) a complex comprising an isolated, recombinant polypeptide comprising:

(a) a sequence of peptide deformylase and DnaK **protein** (gi/9951024);

(b) a sequence of ribosome recycling factor and DNA ligase, NAD-dependent (gi/14972593);

(c) a sequence of translation elongation factor P and ribosomal **protein** L1 (gi/14972107);

(d) a sequence of DnaK **protein** from P. aeruginosa and hsp GrpE (gi/9951026);

(e) a sequence of **protein** chain elongation factor EF-Tu and 50S ribosomal **protein** L13 (gi/9950666), 30S ribosomal **protein** S3 (gi/9950474), 30S ribosomal **protein** S2 (gi/9949817), elongation factor Ts (gi/9949816), or DnaK **protein** (gi/9951024); or

(f) a sequence of **protein** chain elongation factor EF-Ts and translational elongation factor TU (gi/13700439) or 80 kDa unidentified **protein**; and

(6) a host cell comprising a nucleic acid encoding (P), where the culture of the host cell produces 1 mg of the polypeptide/l of culture and the polypeptide is at least one-third soluble as measured by gel electrophoresis.

ACTIVITY - Antibacterial.

MECHANISM OF ACTION - Vaccine; Modulator of (P).

No biological data given.

USE - (I) is useful for designing a modulator for the prevention or treatment of S. aureus, H. pylori, P. aeruginosa, S. pneumoniae or E. coli related disease or disorder. The method comprises providing a three-dimensional (3D) structure for (I), identifying a potential modulator by reference to the 3D structure, contacting the potential modulator with the recombinant polypeptide and assaying the **activity** of the polypeptide or determining the viability of S. aureus, H. pylori, P. aeruginosa, S. pneumoniae or E. coli after contact with the modulator, where a change in the **activity** of the polypeptide or the viability of the bacteria indicates that the modulator may be useful for preventing or treating the disease or disorder. (P) is also useful for identifying small molecules that bind to (P). The method comprises generating a first NMR spectrum of (P) which is isotopically labeled, exposing (P) to one or more small molecules, generating a second NMR spectrum of (P) which has been exposed to one or more small molecules, and comparing the first and second spectra to determine differences between the spectra, where the difference indicates one or more small molecules that have bound to (P) (claimed).

The structural and functional information of (I) aid in the discovery and design of therapeutic and diagnostic molecules. The crystal structure is useful to make a structural or computer model of the polypeptide, complex or its portion. (I) is also useful for determining crystal structure of a homolog of (P). A **protein** complex comprising (P) is useful for identifying modulators of the **protein** complex. Detecting the presence of (P) is useful for diagnosing a patient suffering from a disease or disorder of a pathogenic species. The diagnostic assays are useful for monitoring the effectiveness of an anti-pathogenic treatment in an individual suffering from a disease or disorder of such pathogen. (I) and the recombinant polypeptides are useful for inducing an immunological response in an individual and as an antigen for vaccination of a host to produce specific antibodies which protect against invasion of bacteria, for e.g. by blocking adherence of bacteria to damaged tissue. The polypeptides are also useful for developing antimicrobial agents which are useful as surface disinfectants, topical pharmaceuticals, personal hygiene applications, additive to cell culture medium and systemic pharmaceutical products, and as food preservative or in treating food products to eliminate potential pathogens.

Dwg.0/77

ACCESSION NUMBER: 2003-513596 [48] WPIDS
DOC. NO. CPI: C2003-137529
TITLE: New crystallized recombinant polypeptides from Staphylococcus aureus, Streptococcus pneumoniae, Helicobacter pylori or Pseudomonas aeruginosa involved in general metabolism, useful as drug targets for pathogenic bacteria.
DERWENT CLASS: A96 B04 D16
INVENTOR(S): ALAM, M Z; AWREY, D; BEATTIE, B; CANADIEN, V; DHARAMSI, A; DOMAGALA, M; EDWARDS, A; HOUSTON, S; MANSOURY, K; NECAKOV, S; NETHERY, K; NG, I; PINDER, B; SHELDRICK, B; VALLEE, F; VEDADI, M; WREZEL, O
PATENT ASSIGNEE(S): (AFFI-N) AFFINIUM PHARM INC
COUNTRY COUNT: 101
PATENT INFORMATION:

PATENT NO	KIND	DATE	WEEK	LA	PG
WO 2003044185	A2	20030530	(200348)*	EN	277

RW: AT BE BG CH CY CZ DE DK EA EE ES FI FR GB GH GM GR IE IT KE LS LU MC MW MZ NL OA PT SD SE SK SL SZ TR TZ UG ZM ZW

W: AE AG AL AM AT AU AZ BA BB BG BR BY BZ CA CH CN CO CR CU CZ DE DK DM DZ EC EE ES FI GB GD GE GH GM HR HU ID IL IN IS JP KE KG KP KR KZ LC LK LR LS LT LU LV MA MD MG MK MN MW MX MZ NO NZ OM PH PL PT RO RU SD SE SG SI SK SL TJ TM TN TR TT TZ UA UG US UZ VC VN YU ZA ZM ZW

APPLICATION DETAILS:

PATENT NO	KIND	APPLICATION	DATE
WO 2003044185	A2	WO 2002-CA1768	20021121

PRIORITY APPLN. INFO: US 2001-343679P 20011228; US 2001-332160P 20011121; US 2001-333661P 20011127; US 2001-333665P 20011127; US 2001-341770P 20011218; US 2001-341954P 20011219; US 2001-342003P 20011219; US 2001-342542P 20011220; US 2001-344252P 20011221; US 2001-343570P 20011228; US 2001-343606P 20011228

L5 ANSWER 12 OF 23 WPIDS COPYRIGHT 2003 THOMSON DERWENT on STN

TI Screening drug candidates for use in treating immune system disorders.

AN 2001-638629 [73] WPIDS

AB US2001031462 A UPAB: 20011211

NOVELTY - Screening (I) drug candidates for use in treating immune system disorders, comprising adding a drug candidate to a cell that expresses a specific expression profile gene (G), and determining the effect of the drug candidate on expression of (G), is new.

DETAILED DESCRIPTION - Screening (I) drug candidates for use in treating immune system disorders, comprising adding a drug candidate to a cell that expresses a specific expression profile gene (G), and determining the effect of the drug candidate on expression of (G), is new. (G) is Egr-1, Egr-2, Nur77, c-myc, MIP-1a, MIP-1b,BL34, gfi-1, NAIB2, neurogranin, SLAP, A1, E2-20K, SATB 1, Cctq, kappa V, pcp-4, TGIF, CD83, ApoE, Aeg-2, CD72, cyclin D2, 1ck, MEF-2C, brnk, IgD, Evi-2, vimentin, CD36, c-fes, c-fos, TRAP, hIP30, Ly6E.1, LRG-21, Fos B, gadd153, mafk, Ah-R, C/EBP beta, EZF, TIS7, TIS11, TIS11b, LSIRF, MKP1, PAC-1, PEP, MacMARCKS, SNK, Stral3, kir/gem, EB12, IL1-R2, MyD116, RP105, uPAR, 4F2, hRab3O, Id3, BKLF, LKLF, **EFP**, bcl-3, caspase 2, GILZ, hIFI-204, hRhoH, TRAF5, LT-beta, IFNg-RII, gadd45, CDC47, NAG, scd2, kappa 0 ig, iap38, G7e, B29, or SCD2.

INDEPENDENT CLAIMS are also included for the following:

(1) screening (II) for a bioactive agent capable of binding to a B lymphocyte modulator **protein** (BLMP), comprising combining the BLMP and a candidate bioactive agent, and determining the binding of the candidate agent to the BLMP;

(2) screening (III) for a bioactive agent capable of modulating the **activity** of a B lymphocyte modulator **protein** (BLMP), comprising combining the BLMP and a candidate bioactive agent, and determining the effect of the candidate agent on the bioactivity of the BLMP;

(3) evaluating (IV) the effect of an immunosuppressive drug comprising:

(a) administering the drug to a patient;

(b) removing a cell sample from the patient; and

(c) determining the expression profile of the cell sample; and

(4) an array of probes (V), comprising a support bearing a number of nucleic acid probes complementary to a number of mRNAs expressed by (G).

USE - For the identification and characterization of targets useful in prognosis, monitoring, rational drug design and/or therapeutic intervention of immune system disorders.

Dwg.0/4

ACCESSION NUMBER: 2001-638629 [73] WPIDS
DOC. NO. CPI: C2001-188864
TITLE: Screening drug candidates for use in treating immune system disorders.
DERWENT CLASS: B04 D16
INVENTOR(S): GLYNNE, R; GOODNOW, C; MACK, D
PATENT ASSIGNEE(S): (GLYN-I) GLYNNE R; (GOOD-I) GOODNOW C; (MACK-I) MACK D
COUNTRY COUNT: 1
PATENT INFORMATION:

PATENT NO	KIND	DATE	WEEK	LA	PG
US 2001031462	A1	20011018	(200173)*		41

APPLICATION DETAILS:

PATENT NO	KIND	APPLICATION	DATE
US 2001031462	A1 Provisional	US 1999-171796P	19991222
		US 2000-747760	20001221

PRIORITY APPLN. INFO: US 1999-171796P 19991222; US 2000-747760 20001221

L5 ANSWER 13 OF 23 WPIDS COPYRIGHT 2003 THOMSON DERWENT on STN
TI Identifying a compound which modulates the **activity** of prokaryotic elongation factor p (**efp**) for screening for compounds which can be used as antibiotics comprises contacting **efp** with a compound and determining if **efp** **activity** is modified.
AN 2000-524303 [47] WPIDS
AB WO 200045177 A UPAB: 20000925
NOVELTY - A method (M1) for identifying a compound which modulates the **activity** of **efp** comprises contacting **efp** with a compound and determining whether the compound modifies **activity** of **efp**.

DETAILED DESCRIPTION - INDEPENDENT CLAIMS are also included for the following:

(1) a method (M2) for identifying a compound which modulates **efp activity** comprising:

(a) contacting a cell containing **efp** with a compound identified by M1; and

(b) determining whether the compound inhibits cell growth;

(2) a method (M3) for identifying a compound which modulates **efp activity** comprising:

(a) contacting a composition comprising **efp**, N-formylmethionyl-tRNA (fMet-tRNA), 30S subunit, 50S, an mRNA containing an AUG sequence and initiation factors 1,2 and 3 with a compound; and

(b) determining whether the compound allows fMet-tRNA to bind to a complex formed through the interaction of **efp**, 30S subunit, 50S, an mRNA containing an AUG sequence and initiation factors 1,2 and 3;

(3) a method (M4) for identifying a compound which modulates **efp activity** comprising:

(a) contacting **efp** with prokaryotic 30S subunit or 70S ribosome to form a composition;

(b) contacting the composition with a compound; and

(c) determining whether the compound binds to **efp** in association with the 30S subunit or 70S ribosome or interferes with the binding of **efp** and the 30S subunit or 70S ribosome;

(4) a method (M5) for identifying a compound which modulates **efp activity** comprising:

(a) contacting **efp** with a composition comprising either 50S subunit or 70S ribosome, a tRNA fragment comprising CACCA-radiolabeled amino acid and a peptide bond donor to form a second composition;

(b) contacting the second composition with the compound; and

(c) determining whether the compound inhibits the first peptide bond reaction;

(5) a method (M6) for identifying a compound which modulates **efp activity** comprising:

(a) contacting a cell or composition containing **efp** with a detectably labelled oxazolidinone compound known to bind **efp**;

(b) contacting the composition or cell with an unlabelled compound; and

(c) determining whether the unlabelled compound displaces the labelled oxazolidinone compound from the complex;

(6) a method (M7) for identifying a compound which modulates **efp** but not eukaryotic eIF5A **activity** comprising:

(a) determining whether the compound modulates the **activity** of prokaryotic **efp** by M1 - M7;

(b) contacting eIF5A with a composition comprising methionyl-tRNA (Met-tRNA), 80S ribosome, an mRNA containing an AUG sequence, initiation factors eIF-2, eIF-3, eIF-5, eIF-4C, eIF-4D and a peptide bond donor to form a second composition;

(c) contacting the second composition with a compound; and

(d) determining whether the compound inhibits the first peptide bond reaction of a complex formed through the interaction of eIF5A, Met-tRNA, 80S ribosome, an mRNA containing an AUG sequence, initiation factors eIF-2, eIF-3, eIF-5, eIF-4C and eIF-4D; and

(7) modulating the **activity** of prokaryotic **efp**, the 30S subunit, 50S subunit, 70S ribosome or L16 **protein** comprising contacting the **efp** or cell or cell preparation containing the **efp**, the 30S subunit, 50S subunit, 70S ribosome or L16 **protein** with an oxazolidinone compound.

USE - To screen for compounds which modulate ribosome mediated peptide bond formation. These screening assays can be used to discover new and useful antibiotics.

ADVANTAGE - This screening method is more rapid and direct than currently available methods.

Dwg.0/0

ACCESSION NUMBER: 2000-524303 [47] WPIDS
DOC. NO. NON-CPI: N2000-387540
DOC. NO. CPI: C2000-155724
TITLE: Identifying a compound which modulates the **activity** of prokaryotic elongation factor p (**efp**) for screening for compounds which can be used as antibiotics comprises contacting **efp** with a compound and determining if **efp** **activity** is modified.
DERWENT CLASS: B04 D16 S03
INVENTOR(S): MAROTTI, K R; POORMAN, R A; SHINABARGER, D L; WELLS, P A
PATENT ASSIGNEE(S): (PHAA) PHARMACIA & UPJOHN; (PHAA) PHARMACIA & UPJOHN CO
COUNTRY COUNT: 87
PATENT INFORMATION:

PATENT NO	KIND	DATE	WEEK	LA	PG
WO 2000045177	A1	20000803	(200047)*	EN	52

RW: AT BE CH CY DE DK EA ES FI FR GB GH GM GR IE IT KE LS LU MC MW NL OA PT SD SE SL SZ UG ZW

W: AE AL AM AT AU AZ BA BB BG BR BY CA CH CN CU CZ DE DK EE ES FI GB GD GE GH GM HR HU ID IL IN IS JP KE KG KP KR KZ LC LK LR LS LT LU LV MD MG MK MN MW MX NO NZ PL PT RO RU SD SE SG SI SK SL TJ TM TR TT UA UG US UZ VN YU ZA ZW

AU 9942246 A 20000818 (200057)
EP 1147422 A1 20011024 (200171) EN
R: AL AT BE CH CY DE DK ES FI FR GB GR IE IT LI LT LU LV MC MK NL PT RO SE SI
JP 2002535680 W 20021022 (200301) 63
US 6511813 B1 20030128 (200311)

APPLICATION DETAILS:

PATENT NO	KIND		APPLICATION	DATE
WO 2000045177	A1		WO 1999-US12073	19990528
AU 9942246	A		AU 1999-42246	19990528
EP 1147422	A1		EP 1999-926086	19990528
			WO 1999-US12073	19990528
JP 2002535680	W		WO 1999-US12073	19990528
			JP 2000-596378	19990528
US 6511813	B1	Provisional	US 1999-117473P	19990127
		Div ex	US 1999-322732	19990528
			US 2000-704321	20001102

FILING DETAILS:

PATENT NO	KIND		PATENT NO
AU 9942246	A	Based on	WO 2000045177
EP 1147422	A1	Based on	WO 2000045177
JP 2002535680	W	Based on	WO 2000045177

PRIORITY APPLN. INFO: US 1999-117473P 19990127; US 1999-322732 19990528; US 2000-704321 20001102

L5 ANSWER 14 OF 23 MEDLINE on STN

TI Cell cycle regulatory E3 ubiquitin ligases as anticancer targets.

AB Disregulation of the cell cycle and proliferation play key roles in cellular transformation and tumorigenesis. Such processes are intimately tied to the concentration, localization and **activity** of enzymes, adapters, receptors, and structural proteins in cells. Ubiquitination of these cellular regulatory proteins, governed by specific enzymes in the ubiquitin (Ub) conjugation cascade, has profound effects on their various functions, most commonly through proteasome targeting and degradation. This review will focus on a variety of E3 Ub ligases as potential oncology drug targets, with particular emphasis on the role of these molecules in the regulation of stability, localization, and **activity** of key proteins such as tumor suppressors and oncoproteins. E3 ubiquitin ligases that have established roles in cell cycle and apoptosis, such as the anaphase-promoting complex (APC), the Skp-1-Cul1-F-box class, and the murine double minute 2 (MDM2) **protein**, in addition to more recently discovered E3 ubiquitin ligases which may be similarly important in tumorigenesis, (e.g. Smurf family, CHFR, and **Efp**), will be discussed. We will present evidence to support E3 ligases as good biological targets in the development of anticancer therapeutics and address challenges in drug discovery for these targets.

ACCESSION NUMBER: 2003024782 MEDLINE
DOCUMENT NUMBER: 22419272 PubMed ID: 12531181
TITLE: Cell cycle regulatory E3 ubiquitin ligases as anticancer targets.
AUTHOR: Pray Todd R; Parlati Francesco; Huang Jianing; Wong Brian R; Payan Donald G; Bennett Mark K; Issakani Sarkiz Daniel; Molineaux Susan; Demo Susan D
CORPORATE SOURCE: Rigel Pharmaceuticals, Inc., 240 East Grand Avenue, South San Francisco, California 94080, USA.. tpray@rigel.com
SOURCE: Drug Resist Updat, (2002 Dec) 5 (6) 249-58. Ref: 80
Journal code: 9815369. ISSN: 1368-7646.

PUB. COUNTRY: Scotland: United Kingdom
DOCUMENT TYPE: Journal; Article; (JOURNAL ARTICLE)
General Review; (REVIEW)
(REVIEW, TUTORIAL)
LANGUAGE: English
FILE SEGMENT: Priority Journals
ENTRY MONTH: 200305
ENTRY DATE: Entered STN: 20030118
Last Updated on STN: 20030521
Entered Medline: 20030520

L5 ANSWER 15 OF 23 MEDLINE on STN
TI The chvH locus of Agrobacterium encodes a homologue of an elongation factor involved in **protein** synthesis.
AB The virulence of Agrobacterium tumefaciens depends on both chromosome- and Ti plasmid-encoded gene products. In this study, we characterize a chromosomal locus, chvH, previously identified by TnphoA mutagenesis and shown to be required for tumor formation. Through DNA sequencing and comparison of the sequence with identified sequences in the database, we show that this locus encodes a **protein** similar in sequence to elongation factor P, a **protein** thought to be involved in peptide bond synthesis in Escherichia coli. The analysis of vir-lacZ and vir-phoA translational fusions as well as Western immunoblotting revealed that the expression of Vir proteins such as VirE2 was significantly reduced in the chvH mutant compared with the wild-type strain. The E. coli **efp** gene complemented detergent sensitivity, virulence, and expression of VirE2 in the chvH mutant, suggesting that chvH and **efp** are functionally homologous. As expected, ChvH exerts its **activity** at the posttranscriptional level. Southern analysis suggests that the gene encoding this elongation factor is present as a single copy in A. tumefaciens. We constructed a chvH deletion mutant in which a 445-bp fragment within its coding sequence was deleted and replaced with an omega fragment. On complex medium, this mutant grew more slowly than the wild-type strain, indicating that elongation factor P is important but not essential for the growth of Agrobacterium.
ACCESSION NUMBER: 2001086878 MEDLINE
DOCUMENT NUMBER: 20566665 PubMed ID: 11114898
TITLE: The chvH locus of Agrobacterium encodes a homologue of an elongation factor involved in **protein** synthesis.
AUTHOR: Peng W T; Banta L M; Charles T C; Nester E W
CORPORATE SOURCE: Department of Microbiology, University of Washington, Seattle, Washington 98195-7242, USA.
CONTRACT NUMBER: GM32618 (NIGMS)
SOURCE: JOURNAL OF BACTERIOLOGY, (2001 Jan) 183 (1) 36-45.
Journal code: 2985120R. ISSN: 0021-9193.
PUB. COUNTRY: United States
DOCUMENT TYPE: Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
OTHER SOURCE: GENBANK-AF177860
ENTRY MONTH: 200101
ENTRY DATE: Entered STN: 20010322
Last Updated on STN: 20010322
Entered Medline: 20010118

L5 ANSWER 16 OF 23 MEDLINE on STN
TI A novel baculovirus envelope fusion **protein** with a proprotein convertase cleavage site.
AB The entry mechanism of Spodoptera exigua multicapsid nucleopolyhedrovirus (SeMNPV), a group II NPV, in cultured cells was examined. SeMNPV budded virus (BV) enters by endocytosis as do the BVs of the group I NPVs, Autographa californica (Ac) MNPV and Orgyia pseudotsugata (Op) MNPV. In group I NPVs, upon infection acidification of the endosome triggers fusion of the viral and endosomal membrane, which is mediated by the BV envelope

glycoprotein GP64. However, the SeMNPV genome lacks a homolog of GP64 envelope fusion **protein** (**EFP**). A functional homolog of the OpMNPV GP64 **EFP** was identified in SeMNPV ORF8 (Se8; 76 kDa) and appeared to be the major BV envelope **protein**. Surprisingly, a 60-kDa cleavage product of this **protein** is present in the BV envelope. A furin-like proprotein convertase cleavage site (R-X-K/R-R) was identified immediately upstream of the N-terminus of the mature Se8 **protein** and this site was also conserved in the Lymantria dispar (Ld) MNPV homolog (Ld130) of Se8. Syncytium formation assays showed that Se8 and Ld130 alone were sufficient to mediate membrane fusion upon acidification of the medium. Furthermore, C-terminal GFP-fusion proteins of Se8 and Ld130 were primarily localized in the plasma membrane of insect cells. This is consistent with their fusogenic **activity** and supports the conclusion that the Se8 gene product is a functional homolog of the GP64 **EFP**.

ACCESSION NUMBER: 2000465932 MEDLINE
DOCUMENT NUMBER: 20473922 PubMed ID: 11017785
TITLE: A novel baculovirus envelope fusion **protein** with a proprotein convertase cleavage site.
AUTHOR: IJkel W F; Westenberg M; Goldbach R W; Blissard G W; Vlak J M; Zuidema D
CORPORATE SOURCE: Laboratory of Virology, Wageningen University and Research Center, Binnenhaven 11, 6709 PD Wageningen, The Netherlands.
SOURCE: VIROLOGY, (2000 Sep 15) 275 (1) 30-41. Journal code: 0110674. ISSN: 0042-6822.
PUB. COUNTRY: United States
DOCUMENT TYPE: Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
ENTRY MONTH: 200010
ENTRY DATE: Entered STN: 20010322
Last Updated on STN: 20010322
Entered Medline: 20001031

L5 ANSWER 17 OF 23 MEDLINE on STN
TI **Efp** as a primary estrogen-responsive gene in human breast cancer.
AB We have previously isolated the **efp** (estrogen-responsive finger **protein**) that is required for the normal estrogen-induced cell proliferation. Here, we show the genomic organization of the human **efp** gene which consists of nine exons. The **efp** mRNA was expressed in human breast tumors and the estrogen-induced expression of the **efp** was found in MCF-7 human breast cancer cells. Moreover, **efp** promoter **activity** was enhanced through the estrogen-responsive element dependent on estrogen and estrogen receptor. These results suggest that the **efp** can mediate estrogen actions such as cell growth in human breast cancer as a primary responsive gene.

ACCESSION NUMBER: 2000245431 MEDLINE
DOCUMENT NUMBER: 20245431 PubMed ID: 10781795
TITLE: **Efp** as a primary estrogen-responsive gene in human breast cancer.
AUTHOR: Ikeda K; Orimo A; Higashi Y; Muramatsu M; Inoue S
CORPORATE SOURCE: Department of Biochemistry, Saitama Medical School, 38 Morohongo, Moroyama, Iruma-gun, Saitama, Japan.
SOURCE: FEBS LETTERS, (2000 Apr 21) 472 (1) 9-13. Journal code: 0155157. ISSN: 0014-5793.
PUB. COUNTRY: Netherlands
DOCUMENT TYPE: Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
ENTRY MONTH: 200006
ENTRY DATE: Entered STN: 20000616

Last Updated on STN: 20000616
Entered Medline: 20000602

L5 ANSWER 18 OF 23 MEDLINE on STN
TI Estrogen-responsive RING finger mRNA induction in gastrointestinal carcinoma cells following bile acid treatment.
AB The underlying molecular mechanisms of the tumor-promoting **activity** of bile acids such as chenodeoxycholic acid (CDCA) and deoxycholic acid (DCA) and the protective effect of ursodeoxycholic acid (UDCA) remain largely unclear. Using RNA arbitrarily primed PCR (RAP-PCR) for differential display, we identified, cloned and sequenced differentially expressed transcripts after treating gastric carcinoma cells (St 23132) with the bile acids CDCA, DCA and UDCA. One of these transcripts was identified to be an estrogen-responsive RING finger **protein** (**efp**) mRNA. The differential expression of **efp** in gastric cancer cells was confirmed by low stringency RT-PCR. **efp** mRNA levels were induced 3-fold in gastric carcinoma cells after CDCA and DCA treatment, whereas no change in expression was detected after UDCA treatment. Finally, treatment of the colon carcinoma cell line HT 29 with DCA resulted in a 2- to 5-fold induction of **efp** mRNA levels whereas UDCA did not induce **efp**. As expected, **efp** expression was also increased after 24 h of estrogen treatment. In summary, a synergy or a common pathway of tumor enhancement of bile acids and estrogen via **efp** in gastrointestinal carcinogenesis can be envisioned.
ACCESSION NUMBER: 1999070642 MEDLINE
DOCUMENT NUMBER: 99070642 PubMed ID: 9855000
TITLE: Estrogen-responsive RING finger mRNA induction in gastrointestinal carcinoma cells following bile acid treatment.
AUTHOR: Jung B; Vogt T; Mathieu-Daude F; Welsh J; McClelland M; Trenkle T; Weitzel C; Kullmann F
CORPORATE SOURCE: Sidney Kimmel Cancer Center, San Diego, CA 92121, USA.
SOURCE: CARCINOGENESIS, (1998 Nov) 19 (11) 1901-6.
Journal code: 8008055. ISSN: 0143-3334.
PUB. COUNTRY: ENGLAND: United Kingdom
DOCUMENT TYPE: Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
ENTRY MONTH: 199812
ENTRY DATE: Entered STN: 19990115
Last Updated on STN: 19990115
Entered Medline: 19981223

L5 ANSWER 19 OF 23 MEDLINE on STN
TI Promoter analysis of mouse estrogen-responsive finger **protein** (**efp**) gene: mouse **efp** promoter contains an E-box that is also conserved in human.
AB The estrogen-responsive finger **protein** (**efp**) containing a RING finger motif has been identified as an estrogen-responsive gene in human and mouse. Here, we have characterized the basal promoter region of the mouse **efp** gene. The promoter lacks the TATA motif, and transcription initiation sites are found at positions -38T, -64A and -73C from the translation initiation site. Deletion analysis of the 5'-flanking region using Jyg-Mc(B) mouse breast cancer cells indicates that the sequence encompassing from -139 to -1 has a basal transcription **activity**. This region is GC-rich in both mouse and human promoters, and the E-box is precisely matched on the sequence alignment. A mutation experiment with E-box shows that the E-box is functionally active. An electrophoretic mobility shift assay using Jyg-Mc(B) nuclear extracts shows that a transcription factor, USF-1 binds to the E-box in the mouse **efp** promoter. It has been shown that the E-box in the human **efp** promoter is indispensable for basal transcriptional **activity** and binds USF-1. These findings

suggest that the mouse **efp** promoter is regulated by a similar mechanism to that of the human. In mouse, however, we have not found a negative regulatory region that is present in human promoter.

ACCESSION NUMBER: 1998382584 MEDLINE
DOCUMENT NUMBER: 98382584 PubMed ID: 9714786
TITLE: Promoter analysis of mouse estrogen-responsive finger **protein** (**efp**) gene: mouse **efp** promoter contains an E-box that is also conserved in human.
AUTHOR: Ikeda K; Inoue S; Orimo A; Tsutsumi K; Muramatsu M
CORPORATE SOURCE: Department of Biochemistry, Saitama Medical School, Moroyama, Saitama 350-04, Japan.
SOURCE: GENE, (1998 Aug 17) 216 (1) 155-62.
Journal code: 7706761. ISSN: 0378-1119.
PUB. COUNTRY: Netherlands
DOCUMENT TYPE: Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
ENTRY MONTH: 199810
ENTRY DATE: Entered STN: 19981020
Last Updated on STN: 19981020
Entered Medline: 19981005

L5 ANSWER 20 OF 23 MEDLINE on STN
TI The gene encoding the elongation factor P **protein** is essential for viability and is required for **protein** synthesis.
AB Elongation factor P (**EFP**) is a **protein** that stimulates the peptidyltransferase **activity** of fully assembled 70 S prokaryotic ribosomes and enhances the synthesis of certain dipeptides initiated by N-formylmethionine. This reaction appears conserved throughout species and is promoted in eukaryotic cells by a homologous **protein**, eIF5A. Here we ask whether the Escherichia coli gene encoding **EFP** is essential for cell viability. A kanamycin resistance (KanR) gene was inserted near the N-terminal end of the **efp** gene and was cloned into a plasmid, pMAK705, that has a temperature-sensitive origin of replication. After transformation into a recA+ E. coli strain, temperature-sensitive mutants were isolated, and their chromosomal DNA was sequenced. Mutants containing the **efp** -KanR gene in the chromosome grew at 33 degrees C only in the presence of the wild-type copy of the **efp** gene in the pMAK705 plasmid and were unable to grow at 44 degrees C. Incorporation of various isotopes in vivo suggests that translation is impaired in the **efp** mutant at 44 degrees C. At 44 degrees C, mutant cells are severely defective in peptide-bond formation. We conclude that the **efp** gene is essential for cell viability and is required for **protein** synthesis.

ACCESSION NUMBER: 1998070395 MEDLINE
DOCUMENT NUMBER: 98070395 PubMed ID: 9405429
TITLE: The gene encoding the elongation factor P **protein** is essential for viability and is required for **protein** synthesis.
AUTHOR: Aoki H; Dekany K; Adams S L; Ganoza M C
CORPORATE SOURCE: Banting and Best Department of Medical Research, Nucleic Acids, Protein Synthesis and Molecular Genetics, University of Toronto, Toronto, Ontario M5G 1L6, Canada.
SOURCE: JOURNAL OF BIOLOGICAL CHEMISTRY, (1997 Dec 19) 272 (51) 32254-9.
Journal code: 2985121R. ISSN: 0021-9258.
PUB. COUNTRY: United States
DOCUMENT TYPE: Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
ENTRY MONTH: 199801
ENTRY DATE: Entered STN: 19980130
Last Updated on STN: 19980130

Entered Medline: 19980122

L5 ANSWER 21 OF 23 MEDLINE on STN
TI Multiple regulatory elements and binding proteins of the 5'-flanking region of the human estrogen-responsive finger **protein** (**efp**) gene.
AB The **efp**, a member of the RING finger family, was previously identified as an estrogen responsive gene. Here, we characterized basal promoter of the human **efp** gene. Transcription initiation site was found at position -60 G relative to the site for translation initiation, and TATA motif was absent. Deletion and mutation analyses of the 5'-flanking region using MCF-7 breast cancer cells indicated that the sequences located at -137 to -72 had the promoter **activity** for which an E-box (CACGTG) element at -110 to -105 was essential. EMSA showed that USF-1 bound to the E-box and that a **protein**-DNA complex was formed at the positive regulatory region (-137 to -110). Moreover, a strong negative regulatory region was present in -235 to -174. These findings suggest that the human **efp** promoter is regulated by multiple elements and their interacting factors, and the E-box near the transcription initiation site is essential for the basal promoter **activity**.

ACCESSION NUMBER: 97396176 MEDLINE
DOCUMENT NUMBER: 97396176 PubMed ID: 9245730
TITLE: Multiple regulatory elements and binding proteins of the 5'-flanking region of the human estrogen-responsive finger **protein** (**efp**) gene.
AUTHOR: Ikeda K; Inoue S; Orimo A; Sano M; Watanabe T; Tsutsumi K; Muramatsu M
CORPORATE SOURCE: Department of Biochemistry, Saitama Medical School, Moroyama, Japan.
SOURCE: BIOCHEMICAL AND BIOPHYSICAL RESEARCH COMMUNICATIONS, (1997 Jul 30) 236 (3) 765-71.
Journal code: 0372516. ISSN: 0006-291X.
PUB. COUNTRY: United States
DOCUMENT TYPE: Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
OTHER SOURCE: GENBANK-AB003265
ENTRY MONTH: 199709
ENTRY DATE: Entered STN: 19970926
Last Updated on STN: 19970926
Entered Medline: 19970915

L5 ANSWER 22 OF 23 MEDLINE on STN
TI Identification of a membrane fusion domain and an oligomerization domain in the baculovirus GP64 envelope fusion **protein**.
AB The baculovirus GP64 envelope fusion **protein** (GP64 **EFP**) is the major envelope glycoprotein of the budded virion and has been shown to mediate acid-triggered membrane fusion both in virions and when expressed alone in transfected cells. Using site-directed mutagenesis and functional assays for oligomerization, transport, and membrane fusion, we localized two functional domains of GP64 **EFP**. To identify a fusion domain in the GP64 **EFP** of the Orgyia pseudotsugata multiple nuclear polyhedrosis virus (OpMNPV), we examined two hydrophobic regions in the GP64 **EFP** ectodomain. Hydrophobic region I (amino acids 223 to 228) is a cluster of 6 hydrophobic amino acids exhibiting the highest local hydrophobicity in the ectodomain. Hydrophobic region II (amino acids 330 to 338) lies within a conserved region of GP64 **EFP** that contains a heptad repeat of leucine residues and is predicted to form an amphipathic alpha-helix. In region I, nonconservative amino acid substitutions at Leu-226 and Leu-227 (at the center of the hydrophobic cluster) completely abolished fusion **activity** but did not prevent GP64 **EFP** oligomerization or surface localization. To confirm the role of region I in membrane fusion

activity, we used a synthetic 21-amino-acid peptide to generate polyclonal antibodies against region I and demonstrated that antipeptide antibodies were capable of both neutralizing membrane fusion **activity** and reducing infectivity of the virus. In hydrophobic region II, mutations were designed to disrupt several structural characteristics: a heptad repeat of leucine, a predicted alpha-helix, or the local hydrophobicity along one face of the helix. Single alanine substitutions for heptad leucines did not prevent oligomerization, transport, or fusion **activity**. However, multiple alanine substitutions or proline (helix-destabilizing) substitutions disrupted both oligomerization and transport of GP64 **EFP**. In addition, a deletion that removed region II and the predicted alpha-helix was defective for oligomerization, whereas a larger deletion that retained region II and the predicted helix was oligomerized. These results indicate that region II is required for oligomerization and transport and suggest that the predicted helical structure of this region may be important for this function. Thus, by using mutagenesis, functional assays, and antibody inhibition, two functional domains were localized within the baculovirus GP64 **EFP**: a fusion domain located at amino acids 223 to 228 and an oligomerization domain located at amino acids 327 to 335 within a predicted amphipathic alpha-helix.

ACCESSION NUMBER: 95191039 MEDLINE
DOCUMENT NUMBER: 95191039 PubMed ID: 7533858
TITLE: Identification of a membrane fusion domain and an oligomerization domain in the baculovirus GP64 envelope fusion **protein**.
AUTHOR: Monsma S A; Blissard G W
CORPORATE SOURCE: Boyce Thompson Institute for Plant Research, Cornell University, Ithaca, New York 14853-1801.
CONTRACT NUMBER: AI 33657 (NIAID)
SOURCE: JOURNAL OF VIROLOGY, (1995 Apr) 69 (4) 2583-95. Journal code: 0113724. ISSN: 0022-538X.
PUB. COUNTRY: United States
DOCUMENT TYPE: Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
ENTRY MONTH: 199504
ENTRY DATE: Entered STN: 19950425
Last Updated on STN: 19960129
Entered Medline: 19950410

L5 ANSWER 23 OF 23 MEDLINE on STN
TI Overlapping TATA-dependent and TATA-independent early promoter activities in the baculovirus gp64 envelope fusion **protein** gene.
AB In previous studies to characterize basal and activated transcription from the early promoter of the gp64 envelope fusion **protein** (**efp**) gene of the Orgyia pseudotsugata multicapsid nuclear polyhedrosis virus, the TATA box was identified as a functional element, essential for basal transcription from a minimal promoter construct. In the current study, we used discrete deletions and multiple point mutations that removed the functional TATA box from larger promoter constructs of the gp64 **efp** gene to reveal an overlapping TATA-independent transcriptional **activity**. TATA-independent transcriptional **activity** was inhibited in vitro by alpha-amanitin but not by tagetitoxin, demonstrating that like the TATA-dependent **activity** , the TATA-independent **activity** is mediated by RNA polymerase II. Using constructs in which the TATA box (TATATAA) was destroyed by substitution mutations, we identified four elements that are required for the TATA-independent **activity**. Two of the required elements, GATA (at -114) and CACGTG (at -104), were previously shown to specifically bind host transcription factors and activate transcription from the TATA-dependent wild-type gp64 **efp** promoter. The role of the early start site consensus CAGT sequence in TATA-independent transcription was also examined. Single-nucleotide substitution mutations in the CAGT

sequence indicated that certain nucleotides within the CAGT start site were essential. In addition to the start site sequence and two upstream elements, a fourth essential element was identified in the 5' untranslated leader region (5'UTR). While the 5'UTR was not necessary for TATA-dependent transcription, deletion of a 10-bp 5'UTR sequence resulted in the loss of TATA-independent transcriptional **activity**. Although necessary, neither the GATA, CACGTG, start site region, nor 5'UTR element was alone sufficient for accurately initiated TATA-independent transcription from the consensus CAGT start site. Thus, the gp64 **efp** early promoter contains overlapping TATA-dependent and TATA-independent transcriptional activities. A number of common sequence elements (GATA, CACGTG, and start site CAGT) are involved in both of these activities, while one element (in the 5'UTR) is required only in the TATA-independent context.

ACCESSION NUMBER: 95156569 MEDLINE
DOCUMENT NUMBER: 95156569 PubMed ID: 7853477
TITLE: Overlapping TATA-dependent and TATA-independent early promoter activities in the baculovirus gp64 envelope fusion **protein** gene.
AUTHOR: Kogan P H; Chen X; Blissard G W
CORPORATE SOURCE: Boyce Thompson Institute, Cornell University, Ithaca, New York 14853-1801.
CONTRACT NUMBER: AI31130 (NIAID)
SOURCE: JOURNAL OF VIROLOGY, (1995 Mar) 69 (3) 1452-61.
Journal code: 0113724. ISSN: 0022-538X.
PUB. COUNTRY: United States
DOCUMENT TYPE: Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
ENTRY MONTH: 199503
ENTRY DATE: Entered STN: 19950322
Last Updated on STN: 19950322
Entered Medline: 19950313

=> d his

(FILE 'HOME' ENTERED AT 16:17:55 ON 18 NOV 2003)

FILE 'BIOSIS, WPIDS, FSTA, MEDLINE' ENTERED AT 16:18:40 ON 18 NOV 2003
L1 358 S PROKARYOTIC ELONGATION FACTOR P OR EFP
L2 121 S OXAZOLIDINONE COMPOUND
L3 1 S L1 AND L2
L4 81 S EFP AND PROTEIN
L5 23 S L4 AND ACTIVITY

=> s l1 and activity
L6 75 L1 AND ACTIVITY

=> s l1 and fluorescence
L7 4 L1 AND FLUORESCENCE

=> d l7 ti abs ibib tot

L7 ANSWER 1 OF 4 BIOSIS COPYRIGHT 2003 BIOLOGICAL ABSTRACTS INC. on STN
TI Chromosome mapping of human (ZNF147) and mouse genes for estrogen-responsive finger protein (**efp**), a member of the RING finger family.
AB We have previously identified an estrogen-responsive gene, **efp** (estrogen-responsive finger protein), that encodes a putative zinc finger protein (Proc. Natl. Acad. Sci. USA 90:11117-11121,1993). The **efp** protein has a RING finger, a variant type of zinc finger motif, B1 box, and B2 box, each having a pair of zinc fingers, present in a family of apparent DNA-binding proteins. Some members of this family

have transformation capabilities when found in chromosomal translocations. Chromosome mapping of the **efp** gene by **fluorescence** in situ hybridization reveals that human **EFP** (ZNF147) is located at 17q23.1 and that mouse **Efp** is located at 11C. These results provide additional evidence that the mouse 11C region displays conserved synteny with the 17q23.1 region of the human genome.

ACCESSION NUMBER: 1995:171884 BIOSIS
DOCUMENT NUMBER: PREV199598186184
TITLE: Chromosome mapping of human (ZNF147) and mouse genes for estrogen-responsive finger protein (**efp**), a member of the RING finger family.
AUTHOR(S): Inoue, Satoshi; Orimo, Akira; Matsuda, Youichi; Inazawa, Johji; Emi, Mitsuru; Nakamura, Yusuke; Hori, Tada-Aki; Muramatsu, Masami [Reprint author]
CORPORATE SOURCE: Dep. Biochemistry, Saitama Med. Sch., 38 Moro-Hongo, Moroyama-machi, Iruma-gun, Saitama 350-04, Japan
SOURCE: Genomics, (1995) Vol. 25, No. 2, pp. 581-583. CODEN: GNMCEP. ISSN: 0888-7543.
DOCUMENT TYPE: Article
LANGUAGE: English
ENTRY DATE: Entered STN: 26 Apr 1995
Last Updated on STN: 26 Apr 1995

L7 ANSWER 2 OF 4 WPIDS COPYRIGHT 2003 THOMSON DERWENT on STN
TI Identifying a compound which modulates the activity of **prokaryotic elongation factor p** (**efp**) for screening for compounds which can be used as antibiotics comprises contacting **efp** with a compound and determining if **efp** activity is modified.
AN 2000-524303 [47] WPIDS
AB WO 200045177 A UPAB: 20000925
NOVELTY - A method (M1) for identifying a compound which modulates the activity of **efp** comprises contacting **efp** with a compound and determining whether the compound modifies activity of **efp**.

DETAILED DESCRIPTION - INDEPENDENT CLAIMS are also included for the following:

(1) a method (M2) for identifying a compound which modulates **efp** activity comprising:

(a) contacting a cell containing **efp** with a compound identified by M1; and

(b) determining whether the compound inhibits cell growth;

(2) a method (M3) for identifying a compound which modulates **fp** activity comprising:

(a) contacting a composition comprising **efp**, N-formylmethionyl-tRNA (fMet-tRNA), 30S subunit, 50S, an mRNA containing an AUG sequence and initiation factors 1,2 and 3 with a compound; and

(b) determining whether the compound allows fMet-tRNA to bind to a complex formed through the interaction of **efp**, 30S subunit, 50S, an mRNA containing an AUG sequence and initiation factors 1,2 and 3;

(3) a method (M4) for identifying a compound which modulates **efp** activity comprising:

(a) contacting **efp** with prokaryotic 30S subunit or 70S ribosome to form a composition;

(b) contacting the composition with a compound; and

(c) determining whether the compound binds to **efp** in association with the 30S subunit or 70S ribosome or interferes with the binding of **efp** and the 30S subunit or 70S ribosome;

(4) a method (M5) for identifying a compound which modulates **efp** activity comprising:

(a) contacting **efp** with a composition comprising either 50S subunit or 70S ribosome, a tRNA fragment comprising CACCA-radiolabeled amino acid and a peptide bond donor to form a second composition;

(b) contacting the second composition with the compound; and

(c) determining whether the compound inhibits the first peptide bond reaction;

(5) a method (M6) for identifying a compound which modulates **efp** activity comprising:

(a) contacting a cell or composition containing **efp** with a detectably labelled oxazolidinone compound known to bind **efp**;

(b) contacting the composition or cell with an unlabelled compound; and

(c) determining whether the unlabelled compound displaces the labelled oxazolidinone compound from the complex;

(6) a method (M7) for identifying a compound which modulates **efp** but not eukaryotic eIF5A activity comprising:

(a) determining whether the compound modulates the activity of prokaryotic **efp** by M1 - M7;

(b) contacting eIF5A with a composition comprising methionyl-tRNA (Met-tRNA), 80S ribosome, an mRNA containing an AUG sequence, initiation factors eIF-2, eIF-3, eIF-5, eIF-4C, eIF-4D and a peptide bond donor to form a second composition;

(c) contacting the second composition with a compound; and

(d) determining whether the compound inhibits the first peptide bond reaction of a complex formed through the interaction of eIF5A, Met-tRNA, 80S ribosome, an mRNA containing an AUG sequence, initiation factors eIF-2, eIF-3, eIF-5, eIF-4C and eIF-4D; and

(7) modulating the activity of prokaryotic **efp**, the 30S subunit, 50S subunit, 70S ribosome or L16 protein comprising contacting the **efp** or cell or cell preparation containing the **efp** , the 30S subunit, 50S subunit, 70S ribosome or L16 protein with an oxazolidinone compound.

USE - To screen for compounds which modulate ribosome mediated peptide bond formation. These screening assays can be used to discover new and useful antibiotics.

ADVANTAGE - This screening method is more rapid and direct than currently available methods.

Dwg.0/0

ACCESSION NUMBER: 2000-524303 [47] WPIDS
DOC. NO. NON-CPI: N2000-387540
DOC. NO. CPI: C2000-155724
TITLE: Identifying a compound which modulates the activity of **prokaryotic elongation factor p** (**efp**) for screening for compounds which can be used as antibiotics comprises contacting **efp** with a compound and determining if **efp** activity is modified.
DERWENT CLASS: B04 D16 S03
INVENTOR(S): MAROTTI, K R; POORMAN, R A; SHINABARGER, D L; WELLS, P A
PATENT ASSIGNEE(S): (PHAA) PHARMACIA & UPJOHN; (PHAA) PHARMACIA & UPJOHN CO
COUNTRY COUNT: 87
PATENT INFORMATION:

PATENT NO	KIND	DATE	WEEK	LA	PG
WO 2000045177	A1	20000803	(200047)*	EN	52
RW: AT BE CH CY DE DK EA ES FI FR GB GH GM GR IE IT KE LS LU MC MW NL OA PT SD SE SL SZ UG ZW					
W: AE AL AM AT AU AZ BA BB BG BR BY CA CH CN CU CZ DE DK EE ES FI GB GD GE GH GM HR HU ID IL IN IS JP KE KG KP KR KZ LC LK LR LS LT LU LV MD MG MK MN MW MX NO NZ PL PT RO RU SD SE SG SI SK SL TJ TM TR TT UA UG US UZ VN YU ZA ZW					
AU 9942246	A	20000818	(200057)		
EP 1147422	A1	20011024	(200171)	EN	
R: AL AT BE CH CY DE DK ES FI FR GB GR IE IT LI LT LU LV MC MK NL PT RO SE SI					
JP 2002535680	W	20021022	(200301)		63
US 6511813	B1	20030128	(200311)		

APPLICATION DETAILS:

PATENT NO	KIND		APPLICATION	DATE
WO 2000045177	A1		WO 1999-US12073	19990528
AU 9942246	A		AU 1999-42246	19990528
EP 1147422	A1		EP 1999-926086	19990528
			WO 1999-US12073	19990528
JP 2002535680	W		WO 1999-US12073	19990528
			JP 2000-596378	19990528
US 6511813	B1	Provisional	US 1999-117473P	19990127
		Div ex	US 1999-322732	19990528
			US 2000-704321	20001102

FILING DETAILS:

PATENT NO	KIND		PATENT NO
AU 9942246	A	Based on	WO 2000045177
EP 1147422	A1	Based on	WO 2000045177
JP 2002535680	W	Based on	WO 2000045177

PRIORITY APPLN. INFO: US 1999-117473P 19990127; US 1999-322732 19990528; US 2000-704321 20001102

L7 ANSWER 3 OF 4 MEDLINE on STN

TI Transcriptional repression by RING finger protein TIF1 beta that interacts with the KRAB repressor domain of KOX1.

AB Many of the vertebrate zinc finger factors of the Kruppel type (C2H2 zinc fingers) contain in their N-terminus a conserved sequence referred to as the KRAB (Kruppel-associated box) domain that, when tethered to DNA, efficiently represses transcription. Using the yeast two-hybrid system, we have isolated an 835 amino acid RING finger (C3HC4 zinc finger) protein, TIF1 beta (also named KAP-1), that specifically interacts with the KRAB domain of the human zinc finger factor KOX1/ZNF10. TIF1 beta, TIF1 alpha, PML and **efp** belong to a characteristic subgroup of RING finger proteins that contain one or two other Cys/His-rich clusters (B boxes) and a putative coiled-coil in addition to the classical C3HC4 RING finger motif (RBCC configuration). Like TIF1 alpha, TIF1 beta also contains an additional Cys/His cluster (PHD finger) and a bromo-related domain. When tethered to DNA, TIF1 beta can repress transcription in transiently transfected mammalian cells both from promoter-proximal and remote (enhancer) positions, similarly to the KRAB domain itself. We propose that TIF1 beta is a mediator of the transcriptional repression exerted by the KRAB domain.

ACCESSION NUMBER: 97169206 MEDLINE
DOCUMENT NUMBER: 97169206 PubMed ID: 9016654
TITLE: Transcriptional repression by RING finger protein TIF1 beta that interacts with the KRAB repressor domain of KOX1.
AUTHOR: Moosmann P; Georgiev O; Le Douarin B; Bourquin J P; Schaffner W
CORPORATE SOURCE: Institut fur Molekularbiologie der Universitat, Abteilung II, Zurich, Switzerland.
SOURCE: NUCLEIC ACIDS RESEARCH, (1996 Dec 15) 24 (24) 4859-67. Journal code: 0411011. ISSN: 0305-1048.
PUB. COUNTRY: ENGLAND: United Kingdom
DOCUMENT TYPE: Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
OTHER SOURCE: GENBANK-X97548
ENTRY MONTH: 199703
ENTRY DATE: Entered STN: 19970321
Last Updated on STN: 19970321

Entered Medline: 19970311

L7 ANSWER 4 OF 4 MEDLINE on STN
TI Chromosome mapping of human (ZNF147) and mouse genes for estrogen-responsive finger protein (**efp**), a member of the RING *finger family*.
AB We have previously identified an estrogen-responsive gene, **efp** (estrogen-responsive finger protein), that encodes a putative zinc finger protein (Proc. Natl. Acad. Sci. USA 90: 11117-11121, 1993). The **efp** protein has a RING finger, a variant type of zinc finger motif, B1 box, and B2 box, each having a pair of zinc fingers, present in a family of apparent DNA-binding proteins. Some members of this family have transformation capabilities when found in chromosomal translocations. Chromosome mapping of the **efp** gene by **fluorescence** in situ hybridization reveals that human **EFP** (ZNF147) is located at 17q23.1 and that mouse **Efp** is located at 11C. These results provide additional evidence that the mouse 11C region displays conserved synteny with the 17q23.1 region of the human genome.
ACCESSION NUMBER: 95309931 *MEDLINE*
DOCUMENT NUMBER: 95309931 PubMed ID: 7789997
TITLE: Chromosome mapping of human (ZNF147) and mouse genes for estrogen-responsive finger protein (**efp**), a member of the RING finger family.
AUTHOR: Inoue S; Orimo A; Matsuda Y; Inazawa J; Emi M; Nakamura Y; Hori T; Muramatsu M
CORPORATE SOURCE: Department of Biochemistry, Saitama Medical School, Japan.
SOURCE: GENOMICS, (1995 Jan 20) 25 (2) 581-3.
Journal code: 8800135. ISSN: 0888-7543.
PUB. COUNTRY: United States
DOCUMENT TYPE: Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: *Priority Journals*
ENTRY MONTH: 199507
ENTRY DATE: Entered STN: 19950807
Last Updated on STN: 19950807
Entered Medline: 19950721

=> d his

(FILE 'HOME' ENTERED AT 16:17:55 ON 18 NOV 2003)

FILE 'BIOSIS, WPIDS, FSTA, MEDLINE' ENTERED AT 16:18:40 ON 18 NOV 2003
L1 358 S PROKARYOTIC ELONGATION FACTOR P OR EFP
L2 121 S OXAZOLIDINONE COMPOUND
L3 1 S L1 AND L2
L4 81 S EFP AND PROTEIN
L5 23 S L4 AND ACTIVITY
L6 75 S L1 AND ACTIVITY
L7 4 S L1 AND FLUORESCENCE

=> s l7 and l6
L8 1 L7 AND L6

=> d l8 ti abs ibib tot

L8 ANSWER 1 OF 1 WPIDS COPYRIGHT 2003 THOMSON DERWENT on STN
TI *Identifying a compound which modulates the* **activity** of **prokaryotic elongation factor p** (**efp**) for screening for compounds which can be used as antibiotics comprises contacting **efp** with a compound and determining if **efp activity** is modified.
AN 2000-524303 [47] WPIDS
AB WO 200045177 A UPAB: 20000925

NOVELTY - A method (M1) for identifying a compound which modulates the **activity** of **efp** comprises contacting **fp** with a compound and determining whether the compound modifies **activity** of **efp**.

DETAILED DESCRIPTION - INDEPENDENT CLAIMS are also included for the following:

(1) a method (M2) for identifying a compound which modulates **efp activity** comprising:

(a) contacting a cell containing **efp** with a compound identified by M1; and

(b) determining whether the compound inhibits cell growth;

(2) a method (M3) for identifying a compound which modulates **efp activity** comprising:

(a) contacting a composition comprising **efp**, N-formylmethionyl-tRNA (fMet-tRNA), 30S subunit, 50S, an mRNA containing an AUG sequence and initiation factors 1,2 and 3 with a compound; and

(b) determining whether the compound allows fMet-tRNA to bind to a complex formed through the interaction of **efp**, 30S subunit, 50S, an mRNA containing an AUG sequence and initiation factors 1,2 and 3;

(3) a method (M4) for identifying a compound which modulates **efp activity** comprising:

(a) contacting **efp** with prokaryotic 30S subunit or 70S ribosome to form a composition;

(b) contacting the composition with a compound; and

(c) determining whether the compound binds to **efp** in association with the 30S subunit or 70S ribosome or interferes with the binding of **efp** and the 30S subunit or 70S ribosome;

(4) a method (M5) for identifying a compound which modulates **efp activity** comprising:

(a) contacting **efp** with a composition comprising either 50S subunit or 70S ribosome, a tRNA fragment comprising CACCA-radiolabeled amino acid and a peptide bond donor to form a second composition;

(b) contacting the second composition with the compound; and

(c) determining whether the compound inhibits the first peptide bond reaction;

(5) a method (M6) for identifying a compound which modulates **efp activity** comprising:

(a) contacting a cell or composition containing **efp** with a detectably labelled oxazolidinone compound known to bind **efp**;

(b) contacting the composition or cell with an unlabelled compound; and

(c) determining whether the unlabelled compound displaces the labelled oxazolidinone compound from the complex;

(6) a method (M7) for identifying a compound which modulates **efp** but not eukaryotic eIF5A **activity** comprising:

(a) determining whether the compound modulates the **activity** of prokaryotic **efp** by M1 - M7;

(b) contacting eIF5A with a composition comprising methionyl-tRNA (Met-tRNA), 80S ribosome, an mRNA containing an AUG sequence, initiation factors eIF-2, eIF-3, eIF-5, eIF-4C, eIF-4D and a peptide bond donor to form a second composition;

(c) contacting the second composition with a compound; and

(d) determining whether the compound inhibits the first peptide bond reaction of a complex formed through the interaction of eIF5A, Met-tRNA, 80S ribosome, an mRNA containing an AUG sequence, initiation factors eIF-2, eIF-3, eIF-5, eIF-4C and eIF-4D; and

(7) modulating the **activity** of prokaryotic **efp**, the 30S subunit, 50S subunit, 70S ribosome or L16 protein comprising contacting the **efp** or cell or cell preparation containing the **efp**, the 30S subunit, 50S subunit, 70S ribosome or L16 protein with an oxazolidinone compound.

USE - To screen for compounds which modulate ribosome mediated peptide bond formation. These screening assays can be used to discover new and useful antibiotics.

ADVANTAGE - This screening method is more rapid and direct than currently available methods.

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INVENTOR(S): MAROTTI, K R; POORMAN, R A; SHINABARGER, D L; WELLS, P A
PATENT ASSIGNEE(S): (PHAA) PHARMACIA & UPJOHN; (PHAA) PHARMACIA & UPJOHN CO
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WO 2000045177	A1	20000803	(200047)*	EN	52
RW: AT BE CH CY DE DK EA ES FI FR GB GH GM GR IE IT KE LS LU MC MW NL OA PT SD SE SL SZ UG ZW					
W: AE AL AM AT AU AZ BA BB BG BR BY CA CH CN CU CZ DE DK EE ES FI GB GD GE GH GM HR HU ID IL IN IS JP KE KG KP KR KZ LC LK LR LS LT LU LV MD MG MK MN MW MX NO NZ PL PT RO RU SD SE SG SI SK SL TJ TM TR TT UA UG US UZ VN YU ZA ZW					
AU 9942246	A	20000818	(200057)		
EP 1147422	A1	20011024	(200171)	EN	
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JP 2002535680	W	20021022	(200301)		63
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WO 2000045177	A1		WO 1999-US12073	19990528
AU 9942246	A		AU 1999-42246	19990528
EP 1147422	A1		EP 1999-926086	19990528
			WO 1999-US12073	19990528
JP 2002535680	W		WO 1999-US12073	19990528
			JP 2000-596378	19990528
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AU 9942246	A	Based on	WO 2000045177
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JP 2002535680	W	Based on	WO 2000045177

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